

Notice of Allowability

Application No.

09/777,566

Examiner

Delia M. Ramirez

Applicant(s)

SHORT ET AL.

Art Unit

1652

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address--

All claims being allowable, PROSECUTION ON THE MERITS IS (OR REMAINS) CLOSED in this application. If not included herewith (or previously mailed), a Notice of Allowance (PTOL-85) or other appropriate communication will be mailed in due course. **THIS NOTICE OF ALLOWABILITY IS NOT A GRANT OF PATENT RIGHTS.** This application is subject to withdrawal from issue at the initiative of the Office or upon petition by the applicant. See 37 CFR 1.313 and MPEP 1308.

1. ☒ This communication is responsive to 1/22/2007.
2. ☒ The allowed claim(s) is/are 1-13, 16-18, 20-33, 35, 36, 38-43, 45, 46, 82-88 and 92-98.
3. ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some* c) ☐ None of the:
1. ☐ Certified copies of the priority documents have been received.
2. ☐ Certified copies of the priority documents have been received in Application No. _____.
3. ☐ Copies of the certified copies of the priority documents have been received in this national stage application from the International Bureau (PCT Rule 17.2(a)).

* Certified copies not received: _____.

Applicant has THREE MONTHS FROM THE "MAILING DATE" of this communication to file a reply complying with the requirements noted below. Failure to timely comply will result in ABANDONMENT of this application.

THIS THREE-MONTH PERIOD IS NOT EXTENDABLE.

4. ☐ A SUBSTITUTE OATH OR DECLARATION must be submitted. Note the attached EXAMINER'S AMENDMENT or NOTICE OF INFORMAL PATENT APPLICATION (PTO-152) which gives reason(s) why the oath or declaration is deficient.
5. ☐ CORRECTED DRAWINGS (as "replacement sheets") must be submitted.
- (a) ☐ including changes required by the Notice of Draftsperson's Patent Drawing Review (PTO-948) attached
- 1) ☐ hereto or 2) ☐ to Paper No./Mail Date _____.
- (b) ☐ including changes required by the attached Examiner's Amendment / Comment or in the Office action of Paper No./Mail Date _____.
- Identifying indicia such as the application number (see 37 CFR 1.84(c)) should be written on the drawings in the front (not the back) of each sheet. Replacement sheet(s) should be labeled as such in the header according to 37 CFR 1.121(d).
6. ☐ DEPOSIT OF and/or INFORMATION about the deposit of BIOLOGICAL MATERIAL must be submitted. Note the attached Examiner's comment regarding REQUIREMENT FOR THE DEPOSIT OF BIOLOGICAL MATERIAL.

Attachment(s)

- | | |
|-------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------|
| 1. <input type="checkbox"/> Notice of References Cited (PTO-892) | 5. <input type="checkbox"/> Notice of Informal Patent Application |
| 2. <input type="checkbox"/> Notice of Draftsperson's Patent Drawing Review (PTO-948) | 6. <input type="checkbox"/> Interview Summary (PTO-413),
Paper No./Mail Date _____ |
| 3. <input checked="" type="checkbox"/> Information Disclosure Statements (PTO/SB/08),
Paper No./Mail Date <u>6/30/2006</u> | 7. <input checked="" type="checkbox"/> Examiner's Amendment/Comment |
| 4. <input type="checkbox"/> Examiner's Comment Regarding Requirement for Deposit
of Biological Material | 8. <input checked="" type="checkbox"/> Examiner's Statement of Reasons for Allowance |
| | 9. <input type="checkbox"/> Other _____ |

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DETAILED ACTION

Status of the Application

Claims 1-13, 16-33, 35-36, 38-43, 45-46, 81-88, 92-98 are pending.

Amendment of claims 1-2, 8, 10-12, 16, 20, 35-36, 38-43, 46, 81-88, 92-94, 97-98 as submitted in a communication filed on 1/22/2007 is acknowledged.

In a telephone conversation with Mr. Gregory Einhorn on 2/9/2007, an agreement was reached to amend claims 8-9, 35-36, 38-43, 45-46, 82-88, 92-94, 97-98 and cancel claims 19 (no longer referring to a signal peptide as amended by the examiner) and 81 (exact duplicate of claim 46) to place the application in condition for allowance.

Information Disclosure Statement

1. The supplementary partial European search report for EP 02 74 4174 cited in the IDS filed on 6/30/2006 as reference # 3 has been considered by the Examiner.

Examiner's Amendment

2. An Examiner's amendment to the record appears below. Should the changes and/or additions be unacceptable to applicant, an amendment may be filed as provided by 37 CFR 1.312. To ensure consideration of such an amendment, it MUST be submitted no later than the payment of the issue fee.
3. Authorization for this Examiner's amendment was given in a telephone interview with Mr. Gregory Einhorn on 2/9/2007.
4. Please cancel claims 19 and 81.
5. Please replace claims 8-9, 35-36, 38-43, 45-46, 82-88, 92-94, 97-98 as follows:

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8. The expression system of claim 1, wherein the heterologous amino acid sequence encodes a transit peptide.
9. The expression system of claim 1, wherein said heterologous signal sequence encodes a pathogenesis-related (PR) protein PR-S signal peptide from tobacco.
35. A vector comprising a nucleic acid
 - (i) encoding a polypeptide comprising the amino acid sequence of SEQ ID NO:2;
 - (ii) encoding a polypeptide comprising the amino acid sequence of SEQ ID NO:2 from amino acid residue 1 to 432;
 - (iii) encoding a polypeptide (A) comprising the amino acid sequence of SEQ ID NO:2 and lacking a homologous signal sequence, or (B) comprising the amino acid sequence of (A) and further comprising a heterologous signal sequence;
 - (iv) encoding a polypeptide (A) comprising the amino acid sequence of SEQ ID NO:2 from amino acid residue 1 to 432 and lacking a homologous signal sequence, or (B) comprising the amino acid sequence of (A) and further comprising a heterologous signal sequence;
 - (v) encoding a polypeptide comprising the amino acid sequence of (i), (ii), (iii), or (iv), and further comprising a heterologous nucleotide sequence; or
 - (vi) completely complementary to any of the nucleic acids of (i)-(v).
36. An isolated cell comprising a vector comprising a nucleic acid
 - (i) comprising the nucleotide sequence of SEQ ID NO:1;

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- (ii) comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide residue 1 to 1296;
- (iii) comprising (A) the nucleotide sequence of (i) or (ii) lacking a nucleotide sequence encoding a homologous signal sequence, or (B) the nucleotide sequence of (A) and further comprising a nucleotide sequence encoding a heterologous signal sequence;
- (iv) encoding a polypeptide comprising the amino acid sequence of SEQ ID NO:2;
- (v) encoding a polypeptide comprising the amino acid sequence of SEQ ID NO:2 from amino acid residue 1 to 432;
- (vi) encoding (A) the polypeptide of (iv) or (v) lacking a homologous signal sequence, or (B) the polypeptide of (A) and further comprising a nucleotide sequence encoding a heterologous signal sequence;
- (vii) comprising the nucleotide sequence of (i), (ii), or (iii) and further comprising a heterologous nucleotide sequence;
- (viii) encoding the polypeptide of (iv), (v), or (vi) and further comprising a nucleotide sequence encoding a heterologous amino acid sequence; or
- (ix) comprising a nucleotide sequence that is the complete complement of (i), (ii), (iii), or (vii), or the complete complement of the nucleotide sequence encoding the polypeptide of (iv), (v), (vi) or (viii).

38. A cloning vector comprising a nucleic acid

- (i) comprising the nucleotide sequence of SEQ ID NO:1;
- (ii) comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide residue 1 to 1296;

- (iii) comprising (A) the nucleotide sequence of (i) or (ii) lacking a nucleotide sequence encoding a homologous signal sequence, or (B) the nucleotide sequence of (A) and further comprising a nucleotide sequence encoding a heterologous signal sequence;
- (iv) encoding a polypeptide comprising the amino acid sequence of SEQ ID NO:2;
- (v) encoding a polypeptide comprising the amino acid sequence of SEQ ID NO:2 from amino acid residue 1 to 432;
- (vi) encoding (A) the polypeptide of (iv) or (v) lacking a homologous signal sequence, or (B) the polypeptide of (A) and further comprising a nucleotide sequence encoding a heterologous signal sequence;
- (vii) comprising the nucleotide sequence of (i), (ii), or (iii) and further comprising a heterologous nucleotide sequence;
- (viii) encoding the polypeptide of (iv), (v), or (vi) and further comprising a nucleotide sequence encoding a heterologous amino acid sequence; or
- (ix) comprising a nucleotide sequence that is the complete complement of (i), (ii), (iii), or (vii), or the complete complement of the nucleotide sequence encoding the polypeptide of (iv), (v), (vi) or (viii).

39. An expression vector comprising a nucleic acid

- (i) comprising the nucleotide sequence of SEQ ID NO:1;
- (ii) comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide residue 1 to 1296;
- (iii) comprising (A) the nucleotide sequence of (i) or (ii) lacking a nucleotide sequence encoding a homologous signal sequence, or (B) the nucleotide sequence of (A) and further comprising a nucleotide sequence encoding a heterologous signal sequence;

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- (iv) encoding a polypeptide comprising the amino acid sequence of SEQ ID NO:2;
- (v) encoding a polypeptide comprising the amino acid sequence of SEQ ID NO:2 from amino acid residue 1 to 432;
- (vi) encoding (A) the polypeptide of (iv) or (v) lacking a homologous signal sequence, or (B) the polypeptide of (A) and further comprising a nucleotide sequence encoding a heterologous signal sequence;
- (vii) comprising the nucleotide sequence of (i), (ii), or (iii) and further comprising a heterologous nucleotide sequence;
- (viii) encoding the polypeptide of (iv), (v), or (vi) and further comprising a nucleotide sequence encoding a heterologous amino acid sequence; or
- (ix) comprising a nucleotide sequence that is the complete complement of (i), (ii), (iii), or (vii), or the complete complement of the nucleotide sequence encoding the polypeptide of (iv), (v), (vi) or (viii).

40. A bacterial vector comprising a nucleic acid

- (i) comprising the nucleotide sequence of SEQ ID NO:1;
- (ii) comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide residue 1 to 1296;
- (iii) comprising (A) the nucleotide sequence of (i) or (ii) lacking a nucleotide sequence encoding a homologous signal sequence, or (B) the nucleotide sequence of (A) and further comprising a nucleotide sequence encoding a heterologous signal sequence;
- (iv) encoding a polypeptide comprising the amino acid sequence of SEQ ID NO:2;
- (v) encoding a polypeptide comprising the amino acid sequence of SEQ ID NO:2 from amino acid residue 1 to 432;

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- (vi) encoding (A) the polypeptide of (iv) or (v) lacking a homologous signal sequence, or (B) the polypeptide of (A) and further comprising a nucleotide sequence encoding a heterologous signal sequence;
- (vii) comprising the nucleotide sequence of (i), (ii), or (iii) and further comprising a heterologous nucleotide sequence;
- (viii) encoding the polypeptide of (iv), (v), or (vi) and further comprising a nucleotide sequence encoding a heterologous amino acid sequence; or
- (ix) comprising a nucleotide sequence that is the complete complement of (i), (ii), (iii), or (vii), or the complete complement of the nucleotide sequence encoding the polypeptide of (iv), (v), (vi) or (viii).

41. A plasmid comprising a nucleic acid

- (i) comprising the nucleotide sequence of SEQ ID NO:1;
- (ii) comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide residue 1 to 1296;
- (iii) comprising (A) the nucleotide sequence of (i) or (ii) lacking a nucleotide sequence encoding a homologous signal sequence, or (B) the nucleotide sequence of (A) and further comprising a nucleotide sequence encoding a heterologous signal sequence;
- (iv) encoding a polypeptide comprising the amino acid sequence of SEQ ID NO:2;
- (v) encoding a polypeptide comprising the amino acid sequence of SEQ ID NO:2 from amino acid residue 1 to 432;
- (vi) encoding (A) the polypeptide of (iv) or (v) lacking a homologous signal sequence, or (B) the polypeptide of (A) and further comprising a nucleotide sequence encoding a heterologous signal sequence;

- (vii) comprising the nucleotide sequence of (i), (ii), or (iii) and further comprising a heterologous nucleotide sequence;
- (viii) encoding the polypeptide of (iv), (v), or (vi) and further comprising a nucleotide sequence encoding a heterologous amino acid sequence; or
- (ix) comprising a nucleotide sequence that is the complete complement of (i), (ii), (iii), or (vii), or the complete complement of the nucleotide sequence encoding the polypeptide of (iv), (v), (vi) or (viii).

42. A viral particle comprising a nucleic acid

- (i) comprising the nucleotide sequence of SEQ ID NO:1;
- (ii) comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide residue 1 to 1296;
- (iii) comprising (A) the nucleotide sequence of (i) or (ii) lacking a nucleotide sequence encoding a homologous signal sequence, or (B) the nucleotide sequence of (A) and further comprising a nucleotide sequence encoding a heterologous signal sequence;
- (iv) encoding a polypeptide comprising the amino acid sequence of SEQ ID NO:2;
- (v) encoding a polypeptide comprising the amino acid sequence of SEQ ID NO:2 from amino acid residue 1 to 432;
- (vi) encoding (A) the polypeptide of (iv) or (v) lacking a homologous signal sequence, or (B) the polypeptide of (A) and further comprising a nucleotide sequence encoding a heterologous signal sequence;
- (vii) comprising the nucleotide sequence of (i), (ii), or (iii) and further comprising a heterologous nucleotide sequence;

- (viii) encoding the polypeptide of (iv), (v), or (vi) and further comprising a nucleotide sequence encoding a heterologous amino acid sequence; or
- (ix) comprising a nucleotide sequence that is the complete complement of (i), (ii), (iii), or (vii), or the complete complement of the nucleotide sequence encoding the polypeptide of (iv), (v), (vi) or (viii).

43. A phage comprising a nucleic acid

- (i) comprising the nucleotide sequence of SEQ ID NO:1;
- (ii) comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide residue 1 to 1296;
- (iii) comprising (A) the nucleotide sequence of (i) or (ii) lacking a nucleotide sequence encoding a homologous signal sequence, or (B) the nucleotide sequence of (A) and further comprising a nucleotide sequence encoding a heterologous signal sequence;
- (iv) encoding a polypeptide comprising the amino acid sequence of SEQ ID NO:2;
- (v) encoding a polypeptide comprising the amino acid sequence of SEQ ID NO:2 from amino acid residue 1 to 432;
- (vi) encoding (A) the polypeptide of (iv) or (v) lacking a homologous signal sequence, or (B) the polypeptide of (A) and further comprising a nucleotide sequence encoding a heterologous signal sequence;
- (vii) comprising the nucleotide sequence of (i), (ii), or (iii) and further comprising a heterologous nucleotide sequence;
- (viii) encoding the polypeptide of (iv), (v), or (vi) and further comprising a nucleotide sequence encoding a heterologous amino acid sequence; or

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(ix) comprising a nucleotide sequence that is the complete complement of (i), (ii), (iii), or (vii), or the complete complement of the nucleotide sequence encoding the polypeptide of (iv), (v), (vi) or (viii).

45. A recombinant expression system comprising a nucleic acid encoding a phytase enzyme
- (i) having (A) the amino acid sequence of SEQ ID NO:2 lacking a homologous signal sequence, or (B) the amino acid sequence of (A) further comprising a heterologous signal sequence; or
 - (ii) having (A) the amino acid sequence of SEQ ID NO:2 from amino acid residue 1 to 432 lacking a homologous signal sequence, or (B) the amino acid sequence of (A) further comprising a heterologous signal sequence.
46. A method for making a phytase in a cell, wherein the phytase is encoded by an exogenous nucleic acid, comprising culturing the cell under conditions wherein the phytase is expressed,
- wherein the exogenous nucleic acid
- (i) comprises the nucleotide sequence of SEQ ID NO:1;
 - (ii) comprises the nucleotide sequence of SEQ ID NO:1 from nucleotide residue 1 to 1296;
 - (iii) comprises (A) the nucleotide sequence of (i) or (ii) lacking a nucleotide sequence encoding a homologous signal sequence, or (B) the nucleotide sequence of (A) and further comprises a nucleotide sequence encoding a heterologous signal sequence; or
 - (iv) comprises the nucleotide sequence of (i), (ii), or (iii) and a heterologous nucleotide sequence.

82. An expression system for making a polypeptide having phytase activity, comprising an isolated host cell and an exogenous nucleic acid, wherein the exogenous nucleic acid codes for the polypeptide having phytase activity, wherein the isolated host cell is capable of expressing the polypeptide, and the polypeptide having phytase activity

- (i) comprises the amino acid sequence of SEQ ID NO:2;
- (ii) comprises the amino acid sequence of SEQ ID NO:2 from amino acid residue 1 to 432;
- (iii) comprises (A) the amino acid sequence of (i) or (ii), wherein the amino acid sequence lacks a homologous signal sequence, or (B) the amino acid sequence of (A) further comprising a heterologous signal sequence;
- (iv) comprises the amino acid sequence of (i), (ii) or (iii) and a heterologous amino acid sequence; or
- (v) comprises enzymatically active fragments of (i), (ii), (iii) or (iv).

83. A recombinant expression system comprising an isolated host cell comprising a variant nucleic acid encoding a polypeptide having phytase activity, wherein the variant nucleic acid

- (1) encodes a polypeptide
 - (i) comprising the amino acid sequence of SEQ ID NO:2 and further comprising at least one conservative amino acid substitution;
 - (ii) comprising the amino acid sequence of SEQ ID NO:2 from amino acid residue 1 to 432 and further comprising at least one conservative amino acid substitution;

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- (iii) comprising (A) the amino acid sequence of SEQ ID NO:2 and further comprising at least one conservative amino acid substitution, wherein the amino acid sequence lacks a homologous signal sequence, or (B) the amino acid sequence of (A) and further comprising a heterologous signal sequence;
- (iv) comprising (A) the amino acid sequence of SEQ ID NO:2 from amino acid residue 1 to 432 and further comprising at least one conservative amino acid substitution, wherein the amino acid sequence lacks a homologous signal sequence, or (B) the amino acid sequence of (A) and further comprising a heterologous signal sequence; or
- (v) comprising the amino acid sequence of (i), (ii), (iii), or (iv), and further comprising a heterologous amino acid sequence;

wherein the conservative amino acid substitution comprises (a) a replacement, one for another, among the aliphatic amino acids Ala, Val, Leu, and Ile, (b) an interchange of the hydroxyl residues Ser and Thr, (c) an exchange of the acidic residues Asp and Glu, (d) a substitution between the amide residues Asn and Gln, (e) an exchange of the basic residues Lys and Arg, (f) a replacement among the aromatic residues Phe, Tyr, or (g) any combination of (a), (b), (c), (d), (e), or (f);

(2) encodes enzymatically active fragments of (1); or

(3) comprises a nucleotide sequence that is the complete complement of the nucleotide sequence encoding the polypeptide of (1) or (2);

wherein the nucleic acid encoding the polypeptide having phytase activity is operably linked to a transcriptional control sequence, and the amino acid sequence of the polypeptide having phytase activity has at least 95% sequence identity to SEQ ID NO:2.

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84. An isolated prokaryotic cell comprising a variant nucleic acid encoding a polypeptide having phytase activity, wherein the variant nucleic acid

(1) encodes a polypeptide

(i) comprising the amino acid sequence of SEQ ID NO:2 and further comprising at least one conservative amino acid substitution;

(ii) comprising the amino acid sequence of SEQ ID NO:2 from amino acid residue 1 to 432 and further comprising at least one conservative amino acid substitution;

(iii) comprising (A) the amino acid sequence of SEQ ID NO:2 and further comprising at least one conservative amino acid substitution, wherein the amino acid sequence lacks a homologous signal sequence, or (B) the amino acid sequence of (A) and further comprising a heterologous signal sequence;

(iv) comprising (A) the amino acid sequence of SEQ ID NO:2 from amino acid residue 1 to 432 and further comprising at least one conservative amino acid substitution, wherein the amino acid sequence lacks a homologous signal sequence, or (B) the amino acid sequence of (A) and further comprising a heterologous signal sequence; or

(v) comprising the amino acid sequence of (i), (ii), (iii), or (iv), and further comprising a heterologous amino acid sequence;

wherein the conservative amino acid substitution comprises (a) a replacement, one for another, among the aliphatic amino acids Ala, Val, Leu, and Ile, (b) an interchange of the hydroxyl residues Ser and Thr, (c) an exchange of the acidic residues Asp and Glu, (d) a substitution between the amide residues Asn and Gln, (e) an exchange of the basic residues Lys

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and Arg, (f) a replacement among the aromatic residues Phe, Tyr, or (g) any combination of (a), (b), (c), (d), (e), or (f);

(2) encodes enzymatically active fragments of (1); or

(3) comprises a nucleotide sequence that is the complete complement of the nucleotide sequence encoding the polypeptide of (1) or (2);

wherein the nucleic acid encoding the polypeptide having phytase activity is operably linked to a transcriptional control sequence, and the amino acid sequence of the polypeptide having phytase activity has at least 95% sequence identity to SEQ ID NO:2.

85. A vector comprising a variant nucleic acid encoding a polypeptide having phytase activity, wherein the variant nucleic acid

(1) encodes a polypeptide

(i) comprising the amino acid sequence of SEQ ID NO:2 and further comprising at least one conservative amino acid substitution;

(ii) comprising the amino acid sequence of SEQ ID NO:2 from amino acid residue 1 to 432 and further comprising at least one conservative amino acid substitution;

(iii) comprising (A) the amino acid sequence of SEQ ID NO:2 and further comprising at least one conservative amino acid substitution, wherein the amino acid sequence lacks a homologous signal sequence, or (B) the amino acid sequence of (A) and further comprising a heterologous signal sequence;

(iv) comprising (A) the amino acid sequence of SEQ ID NO:2 from amino acid residue 1 to 432 and further comprising at least one conservative amino acid substitution, wherein the amino acid sequence lacks a homologous signal

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sequence, or (B) the amino acid sequence of (A) and further comprising a heterologous signal sequence; or

(v) comprising the amino acid sequence of (i), (ii), (iii), or (iv), and further comprising a heterologous amino acid sequence;

wherein the conservative amino acid substitution comprises (a) a replacement, one for another, among the aliphatic amino acids Ala, Val, Leu, and Ile, (b) an interchange of the hydroxyl residues Ser and Thr, (c) an exchange of the acidic residues Asp and Glu, (d) a substitution between the amide residues Asn and Gln, (e) an exchange of the basic residues Lys and Arg, (f) a replacement among the aromatic residues Phe, Tyr, or (g) any combination of (a), (b), (c), (d), (e), or (f);

(2) encodes enzymatically active fragments of (1); or

(3) comprises a nucleotide sequence that is the complete complement of the nucleotide sequence encoding the polypeptide of (1) or (2);

wherein the nucleic acid encoding the polypeptide having phytase activity is operably linked to a transcriptional control sequence, and the amino acid sequence of the polypeptide having phytase activity has at least 95% sequence identity to SEQ ID NO:2.

86. An isolated host cell comprising a vector comprising a variant nucleic acid encoding a polypeptide having phytase activity, wherein the variant nucleic acid

(1) encodes a polypeptide

(i) comprising the amino acid sequence of SEQ ID NO:2 and further comprising at least one conservative amino acid substitution;

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- (ii) comprising the amino acid sequence of SEQ ID NO:2 from amino acid residue 1 to 432 and further comprising at least one conservative amino acid substitution;
- (iii) comprising (A) the amino acid sequence of SEQ ID NO:2 and further comprising at least one conservative amino acid substitution, wherein the amino acid sequence lacks a homologous signal sequence, or (B) the amino acid sequence of (A) and further comprising a heterologous signal sequence;
- (iv) comprising (A) the amino acid sequence of SEQ ID NO:2 from amino acid residue 1 to 432 and further comprising at least one conservative amino acid substitution, wherein the amino acid sequence lacks a homologous signal sequence, or (B) the amino acid sequence of (A) and further comprising a heterologous signal sequence; or
- (v) comprising the amino acid sequence of (i), (ii), (iii), or (iv), and further comprising a heterologous amino acid sequence;

wherein the conservative amino acid substitution comprises (a) a replacement, one for another, among the aliphatic amino acids Ala, Val, Leu, and Ile, (b) an interchange of the hydroxyl residues Ser and Thr, (c) an exchange of the acidic residues Asp and Glu, (d) a substitution between the amide residues Asn and Gln, (e) an exchange of the basic residues Lys and Arg, (f) a replacement among the aromatic residues Phe, Tyr, or (g) any combination of (a), (b), (c), (d), (e), or (f);

- (2) encodes enzymatically active fragments of (1); or
- (3) comprises a nucleotide sequence that is the complete complement of the nucleotide sequence encoding the polypeptide of (1) or (2);

wherein the nucleic acid encoding the polypeptide having phytase activity is operably linked to a transcriptional control sequence, and the amino acid sequence of the polypeptide having phytase activity has at least 95% sequence identity to SEQ ID NO:2.

87. An isolated host cell comprising a variant exogenous nucleic acid encoding a polypeptide having phytase activity, wherein the variant nucleic acid

(1) encodes a polypeptide

(i) comprising the amino acid sequence of SEQ ID NO:2 and further comprising at least one conservative amino acid substitution;

(ii) comprising the amino acid sequence of SEQ ID NO:2 from amino acid residue 1 to 432 and further comprising at least one conservative amino acid substitution;

(iii) comprising (A) the amino acid sequence of SEQ ID NO:2 and further comprising at least one conservative amino acid substitution, wherein the amino acid sequence lacks a homologous signal sequence, or (B) the amino acid sequence of (A) and further comprising a heterologous signal sequence;

(iv) comprising (A) the amino acid sequence of SEQ ID NO:2 from amino acid residue 1 to 432 and further comprising at least one conservative amino acid substitution, wherein the amino acid sequence lacks a homologous signal sequence, or (B) the amino acid sequence of (A) and further comprising a heterologous signal sequence; or

(v) comprising the amino acid sequence of (i), (ii), (iii), or (iv), and further comprising a heterologous amino acid sequence;

wherein the conservative amino acid substitution comprises (a) a replacement, one for another, among the aliphatic amino acids Ala, Val, Leu, and Ile, (b) an interchange of the hydroxyl residues Ser and Thr, (c) an exchange of the acidic residues Asp and Glu, (d) a substitution between the amide residues Asn and Gln, (e) an exchange of the basic residues Lys and Arg, (f) a replacement among the aromatic residues Phe, Tyr, or (g) any combination of (a), (b), (c), (d), (e), or (f);

(2) encodes enzymatically active fragments of (1); or

(3) comprises a nucleotide sequence that is the complete complement of the nucleotide sequence encoding the polypeptide of (1) or (2);

wherein the nucleic acid encoding the polypeptide having phytase activity is operably linked to a transcriptional control sequence, and the amino acid sequence of the polypeptide having phytase activity has at least 95% sequence identity to SEQ ID NO:2.

88. An isolated eukaryotic cell comprising a variant nucleic acid encoding a polypeptide having phytase activity, wherein the variant nucleic acid

(1) encodes a polypeptide

(i) comprising the amino acid sequence of SEQ ID NO:2 and further comprising at least one conservative amino acid substitution;

(ii) comprising the amino acid sequence of SEQ ID NO:2 from amino acid residue 1 to 432 and further comprising at least one conservative amino acid substitution;

(iii) comprising (A) the amino acid sequence of SEQ ID NO:2 and further comprising at least one conservative amino acid substitution, wherein the amino

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acid sequence lacks a homologous signal sequence, or (B) the amino acid sequence of (A) and further comprising a heterologous signal sequence;

(iv) comprising (A) the amino acid sequence of SEQ ID NO:2 from amino acid residue 1 to 432 and further comprising at least one conservative amino acid substitution, wherein the amino acid sequence lacks a homologous signal sequence, or (B) the amino acid sequence of (A) and further comprising a heterologous signal sequence; or

(v) comprising the amino acid sequence of (i), (ii), (iii), or (iv), and further comprising a heterologous amino acid sequence;

wherein the conservative amino acid substitution comprises (a) a replacement, one for another, among the aliphatic amino acids Ala, Val, Leu, and Ile, (b) an interchange of the hydroxyl residues Ser and Thr, (c) an exchange of the acidic residues Asp and Glu, (d) a substitution between the amide residues Asn and Gln, (e) an exchange of the basic residues Lys and Arg, (f) a replacement among the aromatic residues Phe, Tyr, or (g) any combination of (a), (b), (c), (d), (e), or (f);

(2) encodes enzymatically active fragments of (1); or

(3) comprises a nucleotide sequence that is the complete complement of the nucleotide sequence encoding the polypeptide of (1) or (2);

wherein the nucleic acid encoding the polypeptide having phytase activity is operably linked to a transcriptional control sequence, and the amino acid sequence of the polypeptide having phytase activity has at least 95% sequence identity to SEQ ID NO:2.

92. An expression system comprising a nucleic acid:

(i) comprising the nucleotide sequence of SEQ ID NO:1;

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- (ii) comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide residue 1 to 1296;
- (iii) comprising (A) the nucleotide sequence of (i) or (ii) lacking a nucleotide sequence encoding a homologous signal sequence, or (B) the nucleotide sequence of (A) and further comprising a nucleotide sequence encoding a heterologous signal sequence;
- (iv) encoding a polypeptide comprising the amino acid sequence of SEQ ID NO:2;
- (v) encoding a polypeptide comprising the amino acid sequence of SEQ ID NO:2 from amino acid residue 1 to 432;
- (vi) encoding (A) the polypeptide of (iv) or (v) lacking a homologous signal sequence, or (B) the polypeptide of (A) and further comprising a nucleotide sequence encoding a heterologous signal sequence;
- (vii) comprising the nucleotide sequence of (i), (ii), or (iii) and further comprising a heterologous nucleotide sequence;
- (viii) encoding the polypeptide of (iv), (v), or (vi) and further comprising a nucleotide sequence encoding a heterologous amino acid sequence; or
- (ix) comprising a nucleotide sequence that is the complete complement of (i), (ii), (iii), or (vii), or the complete complement of the nucleotide sequence encoding the polypeptide of (iv), (v), (vi) or (viii).

93. An isolated, synthetic or recombinant nucleic acid:

- (i) comprising the nucleotide sequence of SEQ ID NO:1;
- (ii) comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide residue 1 to 1296;

- (iii) comprising (A) the nucleotide sequence of (i) or (ii) lacking a nucleotide sequence encoding a homologous signal sequence, or (B) the nucleotide sequence of (A) and further comprising a nucleotide sequence encoding a heterologous signal sequence;
- (iv) encoding a polypeptide comprising the amino acid sequence of SEQ ID NO:2;
- (v) encoding a polypeptide comprising the amino acid sequence of SEQ ID NO:2 from amino acid residue 1 to 432;
- (vi) encoding (A) the polypeptide of (iv) or (v) lacking a homologous signal sequence, or (B) the polypeptide of (A) and further comprising a nucleotide sequence encoding a heterologous signal sequence;
- (vii) comprising the nucleotide sequence of (i), (ii), or (iii) and further comprising a heterologous nucleotide sequence;
- (viii) encoding the polypeptide of (iv), (v), or (vi) and further comprising a nucleotide sequence encoding a heterologous amino acid sequence; or
- (ix) comprising a nucleotide sequence that is the complete complement of (i), (ii), (iii), or (vii), or the complete complement of the nucleotide sequence encoding the polypeptide of (iv), (v), (vi) or (viii).

94. A method for glycosylating a polypeptide comprising:
- (a) providing a nucleic acid comprising a sequence encoding a polypeptide having phytase activity to a cell, wherein the nucleic acid has a nucleotide sequence:
 - (i) comprising the nucleotide sequence of SEQ ID NO:1;
 - (ii) comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide residue 1 to 1296;

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- (iii) comprising (A) the nucleotide sequence of (i) or (ii) lacking a nucleotide sequence encoding a homologous signal sequence, or (B) the nucleotide sequence of (A) and further comprising a nucleotide sequence encoding a heterologous signal sequence;
- (iv) encoding a polypeptide comprising the amino acid sequence of SEQ ID NO:2;
- (v) encoding a polypeptide comprising the amino acid sequence of SEQ ID NO:2 from amino acid residue 1 to 432;
- (vi) encoding (A) the polypeptide of (iv) or (v) lacking a homologous signal sequence, or (B) the polypeptide of (A) and further comprising a nucleotide sequence encoding a heterologous signal sequence;
- (vii) comprising the nucleotide sequence of (i), (ii), or (iii) and further comprising a heterologous nucleotide sequence;
- (viii) encoding the polypeptide of (iv), (v), or (vi) and further comprising a nucleotide sequence encoding a heterologous amino acid sequence; or
- (ix) comprising a nucleotide sequence that is the complete complement of (i), (ii), (iii), or (vii), or the complete complement of the nucleotide sequence encoding the polypeptide of (iv), (v), (vi) or (viii); and
- (b) expressing the polypeptide in the cell wherein the cell is capable of glycosylating the polypeptide.

97. An isolated transformed cell or an isolated host cell comprising an exogenous nucleic acid:

- (i) comprising the nucleotide sequence of SEQ ID NO:1;

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- (ii) comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide residue 1 to 1296;
- (iii) comprising (A) the nucleotide sequence of (i) or (ii) lacking a nucleotide sequence encoding a homologous signal sequence, or (B) the nucleotide sequence of (A) and further comprising a nucleotide sequence encoding a heterologous signal sequence;
- (iv) encoding a polypeptide comprising the amino acid sequence of SEQ ID NO:2;
- (v) encoding a polypeptide comprising the amino acid sequence of SEQ ID NO:2 from amino acid residue 1 to 432;
- (vi) encoding (A) the polypeptide of (iv) or (v) lacking a homologous signal sequence, or (B) the polypeptide of (A) and further comprising a nucleotide sequence encoding a heterologous signal sequence;
- (vii) comprising the nucleotide sequence of (i), (ii), or (iii) and further comprising a heterologous nucleotide sequence;
- (viii) encoding the polypeptide of (iv), (v), or (vi) and further comprising a nucleotide sequence encoding a heterologous amino acid sequence; or
- (ix) comprising a nucleotide sequence that is the complete complement of (i), (ii), (iii), or (vii), or the complete complement of the nucleotide sequence encoding the polypeptide of (iv), (v), (vi) or (viii).

98. A vector comprising an exogenous nucleic acid:

- (i) comprising the nucleotide sequence of SEQ ID NO:1;
- (ii) comprising the nucleotide sequence of SEQ ID NO:1 from nucleotide residue 1 to 1296;

- (iii) comprising (A) the nucleotide sequence of (i) or (ii) lacking a nucleotide sequence encoding a homologous signal sequence, or (B) the nucleotide sequence of (A) and further comprising a nucleotide sequence encoding a heterologous signal sequence;
- (iv) encoding a polypeptide comprising the amino acid sequence of SEQ ID NO:2;
- (v) encoding a polypeptide comprising the amino acid sequence of SEQ ID NO:2 from amino acid residue 1 to 432;
- (vi) encoding (A) the polypeptide of (iv) or (v) lacking a homologous signal sequence, or (B) the polypeptide of (A) and further comprising a nucleotide sequence encoding a heterologous signal sequence;
- (vii) comprising the nucleotide sequence of (i), (ii), or (iii) and further comprising a heterologous nucleotide sequence;
- (viii) encoding the polypeptide of (iv), (v), or (vi) and further comprising a nucleotide sequence encoding a heterologous amino acid sequence; or
- (ix) comprising a nucleotide sequence that is the complete complement of (i), (ii), (iii), or (vii), or the complete complement of the nucleotide sequence encoding the polypeptide of (iv), (v), (vi) or (viii).

Reasons for Allowance

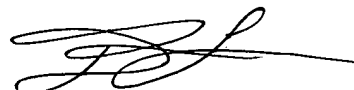
6. The following is an Examiner's statement of reasons for allowance. Although the prior art discloses nucleic acids encoding phytases, the Examiner has found no teaching or suggestion in the prior art directed to the nucleic acid of SEQ ID NO:1 or nucleic acids encoding the polypeptide of SEQ ID NO:2. Therefore, claims 1-13, 16-18, 20-33, 35-36, 38-43, 45-46, 82-88, 92-98 directed to nucleic acids encoding the polypeptide of SEQ ID NO:2 and variants thereof as recited in the claims, host cells and vectors comprising said nucleic acids, a method to recombinantly produce the polypeptides encoded by

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said nucleic acids, and a method for glycosylation of said polypeptides, are allowable over the prior art of record.

Conclusion

7. Claims 1-13, 16-18, 20-33, 35-36, 38-43, 45-46, 82-88, 92-98 are allowed.
8. Any comments considered necessary by applicant must be submitted no later than the payment of the issue fee and, to avoid processing delays, should preferably accompany the issue fee. Such submissions should be clearly labeled "Comments on Statement of Reasons for Allowance."
9. Any inquiry concerning this communication or earlier communications from the examiner should be directed to Delia M. Ramirez whose telephone number is (571) 272-0938. The examiner can normally be reached on Monday-Friday from 8:30 AM to 5:00 PM. If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Dr. Ponnathapura Achutamurthy can be reached on (571) 272-0928. Any inquiry of a general nature or relating to the status of this application or proceeding should be directed to the receptionist whose telephone number is (571) 272-1600.



Delia M. Ramirez, Ph.D.
Patent Examiner
Art Unit 1652

DR
February 12, 2007

DELIA M. RAMIREZ, PH.D.
PRIMARY EXAMINER